



Title: G Proteins, Polynucleotide Encoding the Same and Utilization Thereof

Inventor: Y. Takahashi, *et al.*

Customer No.: 570 Sequence Listing

Atty. Docket No.: 600630-7US (562399)

SEQUENCE LISTING

<110> Sumitomo Chemical Company Limited

<120> NOVEL G PROTEINS, POLYNUCLEOTIDE ENCODING THE SAME AND UTILIZATION THEREOF

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<150> JP 2002/206841

<151> 2002-07-16

<150> JP 2002/367778

<151> 2002-12-19

<150> JP 2003/095955

<151> 2003-03-31

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<212> PRT

<213> Homo sapiens

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35 40 45  
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50 55 60  
Arg Pro Lys Ala Asp Lys Pro Lys Glu Lys Arg Gln Arg Thr Glu Gln  
65 70 75 80  
Leu Ser Ala Glu Glu Arg Glu Ala Ala Lys Glu Arg Glu Ala Val Lys  
85 90 95  
Glu Ala Arg Lys Val Ser Arg Gly Ile Asp Arg Met Leu Arg Asp Gln  
100 105 110  
Lys Arg Asp Leu Gln Gln Thr His Arg Leu Leu Leu Leu Gly Ala Gly  
115 120 125  
Glu Ser Gly Lys Ser Thr Ile Val Lys Gln Met Arg Ile Leu His Val  
130 135 140  
Asn Gly Phe Asn Pro Glu Glu Lys Lys Gln Lys Ile Leu Asp Ile Arg  
145 150 155 160  
Lys Asn Val Lys Asp Ala Ile Val Thr Ile Val Ser Ala Met Ser Thr  
165 170 175  
Ile Ile Pro Pro Val Pro Leu Ala Asn Pro Glu Asn Gln Phe Arg Ser  
180 185 190  
Asp Tyr Ile Lys Ser Ile Ala Pro Ile Thr Asp Phe Glu Tyr Ser Gln  
195 200 205  
Glu Phe Phe Asp His Val Lys Lys Leu Trp Asp Asp Glu Gly Val Lys  
210 215 220  
Ala Cys Phe Glu Arg Ser Asn Glu Tyr Gln Leu Ile Asp Cys Ala Gln  
225 230 235 240  
Tyr Phe Leu Glu Arg Ile Asp Ser Val Ser Leu Val Asp Tyr Thr Pro  
245 250 255  
Thr Asp Gln Asp Leu Leu Arg Cys Arg Val Leu Thr Ser Gly Ile Phe  
260 265 270  
Glu Thr Arg Phe Gln Val Asp Lys Val Asn Phe His Met Phe Asp Val  
275 280 285  
Gly Gly Gln Arg Asp Glu Arg Arg Lys Trp Ile Gln Cys Phe Asn Asp  
290 295 300

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Val Thr Ala Ile Ile Tyr Val Ala Ala Cys Ser Ser Tyr Asn Met Val  
 305 310 315 320  
 Ile Arg Glu Asp Asn Asn Thr Asn Arg Leu Arg Glu Ser Leu Asp Leu  
 325 330 335  
 Phe Glu Ser Ile Trp Asn Asn Arg Trp Leu Arg Thr Ile Ser Ile Ile  
 340 345 350  
 Leu Phe Leu Asn Lys Gln Asp Met Leu Ala Glu Lys Val Leu Ala Gly  
 355 360 365  
 Lys Ser Lys Ile Glu Asp Tyr Phe Pro Glu Tyr Ala Asn Tyr Thr Val  
 370 375 380  
 Pro Glu Asp Ala Thr Pro Asp Ala Gly Glu Asp Pro Lys Val Thr Arg  
 385 390 395 400  
 Ala Lys Phe Phe Ile Arg Asp Leu Phe Leu Arg Ile Ser Thr Ala Thr  
 405 410 415  
 Gly Asp Gly Lys His Tyr Cys Tyr Pro His Phe Thr Cys Ala Val Asp  
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 Thr Glu Asn Ile Arg Arg Val Phe Asn Asp Cys Arg Asp Ile Ile Gln  
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<220>  
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 Ala Pro Ala Pro Ala Leu Ala Pro Val Arg Ala Ala Ala Arg Asp Thr  
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 gcc ccg acc ctg ctc cct cgg ggc ggc gaa ggg agc ccg gca tgc gct 192  
 Ala Arg Thr Leu Leu Pro Arg Gly Gly Glu Gly Ser Pro Ala Cys Ala  
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 cgg ccc aaa gca gac aag ccg aag gag aag ccg cag cgc acc gag cag 240  
 Arg Pro Lys Ala Asp Lys Pro Lys Glu Lys Arg Gln Arg Thr Glu Gln  
 65 70 75 80  
 ctg agt gcc gag gag cgc gag gcg gcc aag gag cgc gag gcg gtc aag 288  
 Leu Ser Ala Glu Glu Arg Glu Ala Ala Lys Glu Arg Glu Ala Val Lys  
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 Glu Ala Arg Lys Val Ser Arg Gly Ile Asp Arg Met Leu Arg Asp Gln  
 100 105 110  
 aag cgc gac ctg cag cag acg cac cgg ctc ctg ctg ctc ggg gct ggt 384  
 Lys Arg Asp Leu Gln Gln Thr His Arg Leu Leu Leu Leu Gly Ala Gly  
 115 120 125

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gag Glu	tct Ser	ggg Gly	aaa Lys	agc Ser	acc Thr	atc Ile	gtc Val	aaa Lys	cag Gln	atg Met	agg Arg	atc Ile	ctg Leu	cac His	gtc Val	432
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275																
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gtc Val	aca Thr	gct Ala	atc Ile	att Ile	tac Tyr	gtc Val	gca Ala	gcc Ala	tgc Cys	agt Ser	agc Ser	tac Tyr	aac Asn	atg Met	gtg Val	960
305																
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att Ile	cga Arg	gaa Glu	gat Asp	aac Asn	aac Asn	acc Thr	aac Asn	agg Arg	ctg Leu	aga Arg	gag Glu	tcc Ser	ctg Leu	gat Asp	ctt Leu	1008
325																
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ttt Phe	gaa Glu	agc Ser	atc Ile	tgg Trp	aac Asn	aac Asn	agg Arg	tgg Trp	tta Leu	cgg Arg	acc Thr	att Ile	tct Ser	atc Ile	atc Ile	1056
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375																
380																

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cct gaa gac gca aca cca gat gca gga gaa gat ccc aaa gtt aca aga 1200  
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385 390 395 400

gcc aag ttc ttt atc cgg gac ctg ttt ttg agg atc agc acg gcc acc 1248  
Ala Lys Phe Phe Ile Arg Asp Leu Phe Leu Arg Ile Ser Thr Ala Thr  
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ggt gac ggc aaa cat tac tgc tac ccg cac ttc acc tgc gcc gtg gac 1296  
Gly Asp Gly Lys His Tyr Cys Tyr Pro His Phe Thr Cys Ala Val Asp  
420 425 430

aca gag aac atc cgc agg gtg ttc aac gac tgc cgc gac atc atc cag 1344  
Thr Glu Asn Ile Arg Arg Val Phe Asn Asp Cys Arg Asp Ile Ile Gln  
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cgg atg cac ctc aag cag tat gag ctc ttg tga 1377  
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<220>  
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<400> 8  
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<400> 9  
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<210> 10  
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<210> 16  
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<212> DNA  
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<210> 17  
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<210> 18  
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<220>  
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 <212> PRT  
 <213> Mus musculus

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 35 40 45  
 Thr Leu Leu Arg Arg Gly Gly Arg Ile Val Ala Asn Ala Arg Pro  
 50 55 60  
 Pro Gly Glu Leu Gln Ser Arg Arg Arg Gln Glu Gln Leu Arg Ala Glu  
 65 70 75 80  
 Glu Arg Glu Ala Ala Lys Glu Ala Arg Lys Val Ser Arg Gly Ile Asp  
 85 90 95  
 Arg Met Leu Arg Glu Gln Lys Arg Asp Leu Gln Gln Thr His Arg Leu  
 100 105 110  
 Leu Leu Leu Gly Ala Gly Glu Ser Gly Lys Ser Thr Ile Val Lys Gln  
 115 120 125  
 Met Arg Ile Leu His Val Asn Gly Phe Asn Pro Glu Glu Lys Lys Gln  
 130 135 140  
 Lys Ile Leu Asp Ile Arg Lys Asn Val Lys Asp Ala Ile Val Thr Ile  
 145 150 155 160  
 Val Ser Ala Met Ser Thr Ile Ile Pro Pro Val Pro Leu Ala Asn Pro  
 165 170 175  
 Glu Asn Gln Phe Arg Ser Asp Tyr Ile Lys Ser Ile Ala Pro Ile Thr  
 180 185 190  
 Asp Phe Glu Tyr Ser Gln Glu Phe Asp His Val Lys Lys Leu Trp  
 195 200 205  
 Asp Asp Glu Gly Val Lys Ala Cys Phe Glu Arg Ser Asn Glu Tyr Gln  
 210 215 220  
 Leu Ile Asp Cys Ala Gln Tyr Phe Leu Glu Arg Ile Asp Ser Val Ser  
 225 230 235 240  
 Leu Val Asp Tyr Thr Pro Thr Asp Gln Asp Leu Leu Arg Cys Arg Val  
 245 250 255  
 Leu Thr Ser Gly Ile Phe Glu Thr Arg Phe Gln Val Asp Lys Val Asn  
 260 265 270  
 Phe His Met Phe Asp Val Gly Gly Gln Arg Asp Glu Arg Arg Lys Trp  
 275 280 285  
 Ile Gln Cys Phe Asn Asp Val Thr Ala Ile Ile Tyr Val Ala Ala Cys  
 290 295 300  
 Ser Ser Tyr Asn Met Val Ile Arg Glu Asp Asn Asn Thr Asn Arg Leu  
 305 310 315 320  
 Arg Glu Ser Leu Asp Leu Phe Glu Ser Ile Trp Asn Asn Arg Trp Leu  
 325 330 335  
 Arg Thr Ile Ser Ile Ile Leu Phe Leu Asn Lys Gln Asp Met Leu Ala  
 340 345 350  
 Glu Lys Val Leu Ala Gly Lys Ser Lys Ile Glu Asp Tyr Phe Pro Glu  
 355 360 365



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Tyr Ala Asn Tyr Thr Val Pro Glu Asp Ala Thr Pro Asp Ala Gly Glu  
 370 375 380  
 Asp Pro Lys Val Thr Arg Ala Lys Phe Phe Ile Arg Asp Leu Phe Leu  
 385 390 395 400  
 Arg Ile Ser Thr Ala Thr Gly Asp Gly Lys His Tyr Cys Tyr Pro His  
 405 410 415  
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 Cys Arg Asp Ile Ile Gln Arg Met His Leu Lys Gln Tyr Glu Leu Leu  
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<210> 26  
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 <212> PRT  
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 35 40 45  
 Val Gly Thr Leu Leu Arg Arg Gly Asp Gly Arg Ile Pro Ala Ser Ala  
 50 55 60  
 Arg Ser Pro Val Glu Leu Gln Asn Arg Arg Arg Gln Glu Gln Leu Arg  
 65 70 75 80  
 Ala Glu Glu Arg Glu Ala Ala Lys Glu Ala Arg Lys Val Ser Arg Gly  
 85 90 95  
 Ile Asp Arg Met Leu Arg Glu Gln Lys Arg Asp Leu Gln Gln Thr His  
 100 105 110  
 Arg Leu Leu Leu Leu Gly Ala Gly Glu Ser Gly Lys Ser Thr Ile Val  
 115 120 125  
 Lys Gln Met Arg Ile Leu His Val Asn Gly Phe Asn Pro Glu Glu Lys  
 130 135 140  
 Lys Gln Lys Ile Leu Asp Ile Arg Lys Asn Val Lys Asp Ala Leu Val  
 145 150 155 160  
 Thr Ile Ile Ser Ala Met Ser Thr Ile Ile Pro Pro Val Pro Leu Ala  
 165 170 175  
 Asn Pro Glu Asn Gln Phe Arg Ser Asp Tyr Ile Lys Ser Ile Ala Pro  
 180 185 190  
 Ile Thr Asp Phe Glu Tyr Ser Gln Glu Phe Phe Asp His Val Lys Lys  
 195 200 205  
 Leu Trp Asp Asp Glu Gly Val Lys Ala Cys Phe Glu Arg Ser Asn Glu  
 210 215 220  
 Tyr Gln Leu Ile Asp Cys Ala Gln Tyr Phe Leu Glu Arg Ile Asp Ser  
 225 230 235 240  
 Val Ser Leu Val Asp Tyr Thr Pro Thr Asp Gln Asp Leu Leu Arg Cys  
 245 250 255  
 Arg Val Leu Thr Ser Gly Ile Phe Glu Thr Arg Phe Gln Val Asp Lys  
 260 265 270  
 Val Asn Phe His Met Phe Asp Val Gly Gly Gln Arg Asp Glu Arg Arg  
 275 280 285  
 Lys Trp Ile Gln Cys Phe Asn Asp Val Thr Ala Ile Tyr Val Ala  
 290 295 300  
 Ala Cys Ser Ser Tyr Asn Met Val Ile Arg Glu Asp Asn Asn Thr Asn  
 305 310 315 320  
 Arg Leu Arg Glu Ser Leu Asp Leu Phe Glu Ser Ile Trp Asn Asn Arg  
 325 330 335  
 Trp Leu Arg Thr Ile Ser Ile Ile Leu Phe Leu Asn Lys Gln Asp Met  
 340 345 350  
 Leu Ala Glu Lys Val Leu Ala Gly Lys Ser Lys Ile Glu Asp Tyr Phe  
 355 360 365

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Pro	Glu	Tyr	Ala	Asn	Tyr	Thr	Val	Pro	Glu	Asp	Ala	Thr	Pro	Asp	Ala
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Gly	Glu	Asp	Pro	Lys	Val	Thr	Arg	Ala	Lys	Phe	Phe	Ile	Arg	Asp	Leu
385					390					395					400
Phe	Leu	Arg	Ile	Ser	Thr	Ala	Thr	Gly	Asp	Gly	Lys	His	Tyr	Cys	Tyr
				405					410					415	
Pro	His	Phe	Thr	Cys	Ala	Val	Asp	Thr	Glu	Asn	Ile	Arg	Arg	Val	Phe
			420					425					430		
Asn	Asp	Cys	Arg	Asp	Ile	Ile	Gln	Arg	Met	His	Leu	Lys	Gln	Tyr	Glu
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Leu	Leu														
	450														

<210> 27  
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 <212> DNA  
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<220>  
 <221> CDS  
 <222> (1)..(1347)

<400> 27	
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Asp Thr Pro Cys Ala Ala Ser Glu Pro Cys Ala Glu Asp Ala Gln Pro	
20 25 30	
agc gcc gcc ccg gcc cct gcc tcg atc cca gcc ccg gct ccc gta ggg	144
Ser Ala Ala Pro Ala Pro Ala Ser Ile Pro Ala Pro Ala Pro Val Gly	
35 40 45	
acc ctg ctc ccg cgt ggc ggc ggc ccg atc gtc gcg aac gcg ccg ccg	192
Thr Leu Leu Arg Arg Gly Gly Gly Arg Ile Val Ala Asn Ala Arg Pro	
50 55 60	
cca ggc gag ctg cag agc cgc ccg cga cag gag cag cta cga gcc gag	240
Pro Gly Glu Leu Gln Ser Arg Arg Arg Gln Glu Gln Leu Arg Ala Glu	
65 70 75 80	
gag cgc gag gcg gct aaa gag gcg agg aaa gtc agc ccg ggc atc gac	288
Glu Arg Glu Ala Ala Lys Glu Ala Arg Lys Val Ser Arg Gly Ile Asp	
85 90 95	
cgc atg ctg cgc gag cag aag ccg gac ctg cag cag acg cac ccg ctc	336
Arg Met Leu Arg Glu Gln Lys Arg Asp Leu Gln Gln Thr His Arg Leu	
100 105 110	
ctg ctg ctg ggg gct ggt gag tcc ggg aaa agc act atc gtc aaa cag	384
Leu Leu Leu Gly Ala Gly Glu Ser Gly Lys Ser Thr Ile Val Lys Gln	
115 120 125	
atg agg atc ctg cac gtc aat ggc ttc aac ccc gag gaa aag aag cag	432
Met Arg Ile Leu His Val Asn Gly Phe Asn Pro Glu Glu Lys Lys Gln	
130 135 140	
aaa att ctg gac atc agg aaa aat gtc aaa gat gcg atc gtg aca atc	480
Lys Ile Leu Asp Ile Arg Lys Asn Val Lys Asp Ala Ile Val Thr Ile	
145 150 155 160	

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Val	Ser	Ala	Met	Ser	Thr	Ile	Ile	Pro	Pro	Val	Pro	Leu	Ala	Asn	Pro	
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gag	aac	cag	ttc	cgg	tca	gat	tat	atc	aag	agc	ata	gcc	cct	atc	act	576
Glu	Asn	Gln	Phe	Arg	Ser	Asp	Tyr	Ile	Lys	Ser	Ile	Ala	Pro	Ile	Thr	
			180					185					190			
gac	ttt	gaa	tat	tcc	cag	gag	ttc	ttt	gac	cat	gtg	aag	aag	ctg	tgg	624
Asp	Phe	Glu	Tyr	Ser	Gln	Glu	Phe	Phe	Asp	His	Val	Lys	Lys	Leu	Trp	
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gac	gat	gaa	gga	gtg	aag	gcc	tgc	ttt	gag	aga	tcc	aac	gag	tac	cag	672
Asp	Asp	Glu	Gly	Val	Lys	Ala	Cys	Phe	Glu	Arg	Ser	Asn	Glu	Tyr	Gln	
	210					215					220					
ctg	atc	gac	tgt	gca	caa	tac	ttc	ctg	gaa	agg	att	gac	agt	gtc	agt	720
Leu	Ile	Asp	Cys	Ala	Gln	Tyr	Phe	Leu	Glu	Arg	Ile	Asp	Ser	Val	Ser	
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Phe	His	Met	Phe	Asp	Val	Gly	Gly	Gln	Arg	Asp	Glu	Arg	Arg	Lys	Trp	
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Ile	Gln	Cys	Phe	Asn	Asp	Val	Thr	Ala	Ile	Ile	Tyr	Val	Ala	Ala	Cys	
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Glu	Lys	Val	Leu	Ala	Gly	Lys	Ser	Lys	Ile	Glu	Asp	Tyr	Phe	Pro	Glu	
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Tyr	Ala	Asn	Tyr	Thr	Val	Pro	Glu	Asp	Ala	Thr	Pro	Asp	Ala	Gly	Glu	
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Asp	Pro	Lys	Val	Thr	Arg	Ala	Lys	Phe	Phe	Ile	Arg	Asp	Leu	Phe	Leu	
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Arg	Ile	Ser	Thr	Ala	Thr	Gly	Asp	Gly	Lys	His	Tyr	Cys	Tyr	Pro	His	
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Asp Ala Pro Cys Glu Asp Ser Glu Pro Cys Ala Glu Asp Ala Gln Pro	
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Ser Ala Ala Pro Ala Pro Ala Pro Ala Pro Ile Pro Ala Pro Ala Pro	
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Val Gly Thr Leu Leu Arg Arg Gly Asp Gly Arg Ile Pro Ala Ser Ala	
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Lys Gln Met Arg Ile Leu His Val Asn Gly Phe Asn Pro Glu Glu Lys	
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145 150 155 160	
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Thr Ile Ile Ser Ala Met Ser Thr Ile Ile Pro Pro Val Pro Leu Ala	

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Ile	Thr	Asp	Phe	Glu	Tyr	Ser	Gln	Glu	Phe	Phe	Asp	His	Val	Lys	Lys	
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Tyr	Gln	Leu	Ile	Asp	Cys	Ala	Gln	Tyr	Phe	Leu	Glu	Arg	Ile	Asp	Ser	
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Val	Ser	Leu	Val	Asp	Tyr	Thr	Pro	Thr	Asp	Gln	Asp	Leu	Leu	Arg	Cys	
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Lys	Trp	Ile	Gln	Cys	Phe	Asn	Asp	Val	Thr	Ala	Ile	Ile	Tyr	Val	Ala	
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Phe	Leu	Arg	Ile	Ser	Thr	Ala	Thr	Gly	Asp	Gly	Lys	His	Tyr	Cys	Tyr	
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cct	cac	ttc	acc	tgc	gcc	gtg	gac	aca	gag	aac	atc	cgc	aga	gtg	ttc	1296

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Pro	His	Phe	Thr	Cys	Ala	Val	Asp	Thr	Glu	Asn	Ile	Arg	Arg	Val	Phe		
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